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TECH CENTER 1600/2900

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/400,802A

DATE: 10/23/2001

TIME: 10:58:36

Input Set : A:\X-11158 Sequence Listing.txt

Output Set : N:\CRF3\10232001\I400802A.raw

3 <110> APPLICANT: Efendic, Suad
 5 <120> TITLE OF INVENTION: USE OF GLP-1 OR ANALOGS IN TREATMENT OF STROKE
 7 <130> FILE REFERENCE: X-11158
 9 <140> CURRENT APPLICATION NUMBER: US 09/400,802A
 10 <141> CURRENT FILING DATE: 1999-09-22
 12 <150> PRIOR APPLICATION NUMBER: US 60/101,719
 13 <151> PRIOR FILING DATE: 1998-09-24
 15 <160> NUMBER OF SEQ ID NOS: 35
 17 <170> SOFTWARE: PatentIn version 3.1

ENTERED

P-5

19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 31
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1
 26 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 27 1 5 10 15
 30 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
 31 20 25 30

34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 28
 36 <212> TYPE: PRT
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: synthetic construct

42 <400> SEQUENCE: 2
 44 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 45 1 5 10 15
 48 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys
 49 20 25

52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 29
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Artificial Sequence
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: synthetic construct

60 <400> SEQUENCE: 3
 62 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 63 1 5 10 15
 66 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly
 67 20 25

70 <210> SEQ ID NO: 4
 71 <211> LENGTH: 30
 72 <212> TYPE: PRT
 73 <213> ORGANISM: Homo sapiens
 75 <400> SEQUENCE: 4
 77 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
 78 1 5 10 15

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81 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
82          20          25          30
85 <210> SEQ ID NO: 5
86 <211> LENGTH: 31
87 <212> TYPE: PRT
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: synthetic construct
93 <400> SEQUENCE: 5
95 His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
96 1          5          10          15
99 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
100          20          25          30
103 <210> SEQ ID NO: 6
104 <211> LENGTH: 31
105 <212> TYPE: PRT
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: synthetic construct
111 <400> SEQUENCE: 6
113 His Ala Gln Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
114 1          5          10          15
117 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
118          20          25          30
121 <210> SEQ ID NO: 7
122 <211> LENGTH: 31
123 <212> TYPE: PRT
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: synthetic construct
129 <220> FEATURE:
130 <221> NAME/KEY: MISC_FEATURE
131 <222> LOCATION: (3)..(3)
132 <223> OTHER INFORMATION: Xaa at position 3 is D-Gln.
135 <400> SEQUENCE: 7
W--> 137 His Ala Xaa Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
138 1          5          10          15
141 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
142          20          25          30
145 <210> SEQ ID NO: 8
146 <211> LENGTH: 31
147 <212> TYPE: PRT
148 <213> ORGANISM: Artificial Sequence
150 <220> FEATURE:
151 <223> OTHER INFORMATION: synthetic construct
153 <400> SEQUENCE: 8
155 His Ala Glu Gly Thr Phe Thr Ser Asp Thr Ser Lys Tyr Leu Glu Gly
156 1          5          10          15
159 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly

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160          20          25          30
163 <210> SEQ ID NO: 9
164 <211> LENGTH: 31
165 <212> TYPE: PRT
166 <213> ORGANISM: Artificial Sequence ✓
168 <220> FEATURE:
169 <223> OTHER INFORMATION: synthetic construct ✓
171 <400> SEQUENCE: 9
173 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Lys Tyr Leu Glu Gly
174 1          5          10          15
177 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
178          20          25          30
181 <210> SEQ ID NO: 10
182 <211> LENGTH: 28
183 <212> TYPE: PRT
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: synthetic construct
189 <220> FEATURE:
190 <221> NAME/KEY: MISC_FEATURE
191 <222> LOCATION: (20)..(20)
192 <223> OTHER INFORMATION: Xaa at position 20 is D-Lys, Gly, Ser, Ala, Leu, Ile, Gln,
Arg, D
193          -Arg and Met;
196 <220> FEATURE:
197 <221> NAME/KEY: MISC_FEATURE
198 <222> LOCATION: (28)..(28)
199 <223> OTHER INFORMATION: Xaa at position 28 is D-Lys, Gly, Ser, Ala, Leu, Ile, Gln,
Arg, D
200          -Arg and Met.
203 <400> SEQUENCE: 10
205 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
206 1          5          10          15
W--> 209 Gln Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Xaa
210          20          25
213 <210> SEQ ID NO: 11
214 <211> LENGTH: 29
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: synthetic construct
221 <220> FEATURE:
222 <221> NAME/KEY: MISC_FEATURE
223 <222> LOCATION: (20)..(20)
224 <223> OTHER INFORMATION: Xaa at position 20 is D-Lys, Gly, Ser, Ala, Leu, Ile, Gln,
Arg, D
225          -Arg and Met;
228 <220> FEATURE:
229 <221> NAME/KEY: MISC_FEATURE
230 <222> LOCATION: (28)..(28)
231 <223> OTHER INFORMATION: Xaa at position 28 is D-Lys, Gly, Ser, Ala, Leu, Ile, Gln,
Arg, D
232          -Arg and Met.

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235 <400> SEQUENCE: 11
237 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
238 1 5 10 15
W--> 241 Gln Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Xaa Gly
242 20 25
245 <210> SEQ ID NO: 12
246 <211> LENGTH: 31
247 <212> TYPE: PRT
248 <213> ORGANISM: Artificial Sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: synthetic construct
253 <220> FEATURE:
254 <221> NAME/KEY: MISC_FEATURE
255 <222> LOCATION: (20)..(20)
256 <223> OTHER INFORMATION: Xaa at position 20 is D-Lys, Gly, Ser, Ala, Leu, Ile, Gln,
Arg, D
257 -Arg and Met;
260 <220> FEATURE:
261 <221> NAME/KEY: MISC_FEATURE
262 <222> LOCATION: (28)..(28)
263 <223> OTHER INFORMATION: Xaa at position 28 is D-Lys, Gly, Ser, Ala, Leu, Ile, Gln,
Arg, D
264 -Arg and Met;
267 <220> FEATURE:
268 <221> NAME/KEY: MISC_FEATURE
269 <222> LOCATION: (30)..(30)
270 <223> OTHER INFORMATION: Xaa at position 30 is Lys, D-Lys, Gly, Ser, Ala, Leu, Ile,
Gln, M
271 et and D-Arg.
274 <400> SEQUENCE: 12
276 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
277 1 5 10 15
W--> 280 Gln Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Xaa Gly Xaa Gly
281 20 25 30
284 <210> SEQ ID NO: 13
285 <211> LENGTH: 31
286 <212> TYPE: PRT
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: synthetic construct
292 <220> FEATURE:
293 <221> NAME/KEY: MISC_FEATURE
294 <222> LOCATION: (10)..(10)
295 <223> OTHER INFORMATION: Xaa at position 10 is Tyr or Val;
298 <220> FEATURE:
299 <221> NAME/KEY: MISC_FEATURE
300 <222> LOCATION: (12)..(12)
301 <223> OTHER INFORMATION: Xaa at position 12 is Lys or Ser;
304 <220> FEATURE:
305 <221> NAME/KEY: MISC_FEATURE
306 <222> LOCATION: (15)..(15)
307 <223> OTHER INFORMATION: Xaa at position 15 is Asp or Glu;

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310 <220> FEATURE:
311 <221> NAME/KEY: MISC_FEATURE
312 <222> LOCATION: (16)..(16)
313 <223> OTHER INFORMATION: Xaa at position 16 is Ser or Gly;
316 <220> FEATURE:
317 <221> NAME/KEY: MISC_FEATURE
318 <222> LOCATION: (17)..(17)
319 <223> OTHER INFORMATION: Xaa at position 17 is Arg or Gln;
322 <220> FEATURE:
323 <221> NAME/KEY: MISC_FEATURE
324 <222> LOCATION: (18)..(18)
325 <223> OTHER INFORMATION: Xaa at position 18 is Arg or Ala;
328 <220> FEATURE:
329 <221> NAME/KEY: MISC_FEATURE
330 <222> LOCATION: (20)..(20)
331 <223> OTHER INFORMATION: Xaa at position 20 is Gln or Lys.
334 <400> SEQUENCE: 13
W--> 336 His Ala Glu Gly Thr Phe Thr Ser Asp Xaa Ser Xaa Tyr Leu Xaa Xaa
337 1 5 10 15
W--> 340 Xaa Xaa Ala Xaa Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
341 20 25 30
344 <210> SEQ ID NO: 14
345 <211> LENGTH: 31
346 <212> TYPE: PRT
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: synthetic construct
352 <400> SEQUENCE: 14
354 Tyr Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
355 1 5 10 15
358 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
359 20 25 30
362 <210> SEQ ID NO: 15
363 <211> LENGTH: 31
364 <212> TYPE: PRT
365 <213> ORGANISM: Artificial Sequence
367 <220> FEATURE:
368 <223> OTHER INFORMATION: synthetic construct
370 <220> FEATURE:
371 <221> NAME/KEY: MISC_FEATURE
372 <222> LOCATION: (1)..(1)
373 <223> OTHER INFORMATION: Xaa at position 1 is N-acetyl-His.
376 <400> SEQUENCE: 15
W--> 378 Xaa Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
379 1 5 10 15
382 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
383 20 25 30
386 <210> SEQ ID NO: 16
387 <211> LENGTH: 31

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\X-11158 Sequence Listing.txt

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L:137 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:336 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20
L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:607 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:817 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:850 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:854 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35